

# **EXHIBIT 14**

## BLAST 2 SEQUENCES

This tool produces the alignment of two given sequences using **BLAST** engine for local alignment.  
The stand-alone executable for blasting two sequences (bl2seq) can be retrieved from NCB1 ftp site

**Reference:** Tatiana A. Tatusova, Thomas L. Madden (1999), "Blast 2 sequences - a new tool for comparing protein and nucleotide sequences", FEMS Microbiol Lett, 174:247-250

Program  blastn  Matrix BL2ONEM62

Parameters used in BLASTN program only:

Reward for a match:  Penalty for a mismatch:

Use Mega BLAST Strand option  Not Applicable

Open gap  and extension gap  penalties

gap x\_dropoff  expect  word size  Filter   Alignments

Sequence 1 Enter accession or GI  or download from file

or sequence in FASTA format from:  to:

```
DYGNSPFYEESTULTHALSSQPTLISSEASLNQLRSUDMFSGLNVPHYGWQGLWSWGWAQTQ  
DPEPASSATITDPKKANRFHRTLLLTLWLPAGYVPSPKHRSPLIANTLWGNMILLATESLKNS  
AELTPSDHPFWGITGGGLGMMVYQEPRENHPGFHMRSSGYFAGMLAGCQHTFSLKFSQTYT  
KLNERYAKNNVSSKNYSQCGEMLFSLQEGFLLAKLVLGLYSYGDHNCHHFYTQGENLTSQGT  
FRSQTMGGAVFFDLPMKPGSTHILTAPFLGALGIYSSLSHFTEVGAYPRSFSTKTPLINV  
LVEIGVKGSFMNATQRQPQAWTVELAYQPVLYRQELEIATQLLASKGIWFGSGSPSSRHAMS  
YKISQQTQPLSWLTLMFQYHGFYSSSTFCNYLNGEIALRF.
```

Sequence 2 Enter accession or GI  or download from file

or sequence in FASTA format from:  to:

```
cttwccaisn rmggygavri arviktavnk eremgeaiaag asgnittstis  
klvertnpay gkhmqdaemf tnaacmtlni wdrfdvfctl gatsgylkgn  
sasfnlvglf gdgvnatkpka adsipnvqln qsvvelytdt tawsvgara  
alwecgcatl gasfqyaqsk pkieelnvca naaeftinkp kgyvgkefpl  
dttagtdaat gtkdasidyh ewqasilsy rlmftpyig vkwrasfds  
dtiriaqpri vtpvvdditl nptiagcgv aganteggis dtmqivslql  
nkmksrkscg iavgttivda dkyavtvetr lideraahvn aqfrf
```

Comments and suggestions to: [blast-help@ncbi.nlm.nih.gov](mailto:blast-help@ncbi.nlm.nih.gov)



## Blast 2 Sequences results

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.3 [Apr-24-2002]

Matrix  gap open:  gap extension:

x\_dropoff:  expect:  wordsize:  Filter  Align

Sequence 1 lcl|seq\_1 Length 955 PMPE PTA-2462

Sequence 2 lcl|seq\_2 Length 394 Mm A

No significant similarity was found

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Program  Blastp  Matrix  BLOSUM62

Parameters used in **BLASTN** program only:

Reward for a match:  Penalty for a mismatch:

Use **Mega BLAST** Strand option  Not Applicable

Open gap  and extension gap  penalties

gap x\_dropoff  expect  word size  Filter  Align

Sequence 1 Enter accession or GI  or download from file

or sequence in FASTA format from:  to:

```
ALSSQPMMLSTSEASLNLQLRSULMDFSGLNVPHYGWQGLWIWGWAKTQDPEFASSATITDPY
KANRFHRTLLLTLWLPAGYVESPWPKHRSPLIANTLWGNMILATESLKNSAELTPSDHPFWGIC
GGGLGMMVYQDPRENHPGFHMRSSGYSAGMIAGQTHTPSLKFQSQTYTKLNERYAKNNVSSK
NYSCQGEMLFLSLQEGFLLTKLVGLSYGDHNCHHFYTQGENLTSQGTFRSQTMGGAVFFDL
PMRPFGSTHILTAPFLGALGIYSSLSHFTEVGAYPRSFSTKTPLINVLVPIGVKGSMNAT
QRPAWTVELAYQPVLVYRQEFGIATQLLASKGIWFGSGSPSSRHAMSYKISQQTQPLSWLT
LHFQYHGFYSSSTFCNYLNGETALRF
```

Sequence 2 Enter accession or GI  or download from file

or sequence in FASTA format from:  to:

```
CTTWCCDAISM RmggygarvI arviktavnk eremgealag asgnittsis
klvertnpay gkhmqdaemf tnaacmtlni wdrfdvfctl gatsgylkgn
sasfnlvglf gdgvnatkpka adsipnvqln qsvvleytdt tawsvgara
alwecgcatalog pkieelnvlc naaeftinkp kgyvgkefpl
ditagtdaat gtkdasidyh ewqaslsisy rlnmftpyig vkwrasafds
dtiriaqprl vtpvvdittl nptiagcgsy aganteggis dtmqivslql
nmkmsrkscg iavgttivda dkyavtvetr lideraahvn aqfrf
```

Comments and suggestions to [blast-help@ncbi.nlm.nih.gov](mailto:blast-help@ncbi.nlm.nih.gov)



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BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.3 [Apr-24-2002]

Matrix  BLOSUM62  gap open:  gap extension:

x\_dropoff:  expect:  wordsize:  Filter  Alignments

Sequence 1 lcl|seq\_1 Length 965 *Sequence 1*

Sequence 2 lcl|seq\_2 Length 394 *momp*

No significant similarity was found